

## SEQUENCE LISTING

<110> LIN, LEU-FEN H

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LILE, JACK

BEKTESH, SUSAN

<120> Glial Cell Line-Derived Neurotrophic Factor

<130> S-225E Rev 070302

<140> 08/182,183

<141> 1994-05-23

<150> 07/764,685

<151> 1991-09-20

<150> 07/774,109

<151> 1991-10-08

<150> 07/788,423

<151> 1991-11-06

<150> 07/855,413

<151> 1992-03-19

<150> PCT/US92/07888

<151> 1992-09-17

<160> 29

C

<170> PatentIn version 3.1

<210> 1

<211> 25

<212> PRT

<213> Rattus rattus

<220>

<221> MISC\_FEATURE

<222> (16)..(16)

<223> Xaa in position 16 may be any one of the 20 naturally occurring amino acids.

<220>

<221> MISC\_FEATURE

<223> N-terminal fragment

<400> 1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Asp | Lys | Gln | Ala | Ala | Ala | Leu | Pro | Arg | Arg | Glu | Arg | Asn | Xaa |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ala | Ala | Ala | Ala | Ser | Pro | Asp | Asn |
|     |     |     | 20  |     |     |     |     | 25  |

<210> 2

<211> 13

<212> PRT

<213> Rattus rattus

<220>

<221> MISC\_FEATURE

<222> (2)..(2)

<223> Xaa in position 2 is either Lys or Gln

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;223&gt; Internal GDNF peptide fragment

&lt;400&gt; 2

Asp Xaa Ile Leu Lys Asn Leu Gly Arg Val Arg Arg Leu  
 1 5 10

&lt;210&gt; 3

&lt;211&gt; 900

&lt;212&gt; DNA

&lt;213&gt; Rattus rattus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (25)..(705)

&lt;223&gt;

&lt;220&gt;

&lt;221&gt; mat\_peptide

&lt;222&gt; (304)..()

&lt;223&gt;

&lt;400&gt; 3

cccccgggct gcaggaattc gggg gtc tac gga gac cgg atc cga ggt gcc 51  
 Val Tyr Gly Asp Arg Ile Arg Gly Ala  
 -90 -85

gcc gcc gga cgg gac tct aag atg aag tta tgg gat gtc gtg gct gtc 99  
 Ala Ala Gly Arg Asp Ser Lys Met Lys Leu Trp Asp Val Val Ala Val  
 -80 -75 -70

tgc ctg gtg ttg ctg cac acc gcg tct gcc ttc ccg ctg ccc gcc ggt 147  
 Cys Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro Ala Gly  
 -65 -60 -55

aag agg ctt ctc gaa gcg ccc gcc gaa gac cac tcc ctc ggc cac cgc 195  
 Lys Arg Leu Leu Glu Ala Pro Ala Glu Asp His Ser Leu Gly His Arg  
 -50 -45 -40

cgc gtg ccc ttc gcg ctg acc agt gac tcc aat atg ccc gaa gat tat 243  
 Arg Val Pro Phe Ala Leu Thr Ser Asp Ser Asn Met Pro Glu Asp Tyr  
 -35 -30 -25

cct gac cag ttt gat gac gtc atg gat ttt att caa gcc acc atc aaa 291  
 Pro Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys  
 -20 -15 -10 -5

aga ctg aaa agg tca cca gat aaa caa gcg gcg gca ctt cct cga aga 339  
 Arg Leu Lys Arg Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg  
 -1 1 5 10

gag agg aac cgg caa gct gca gct gcc agc cca gag aat tcc aga ggg 387  
 Glu Arg Asn Arg Gln Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly  
 15 20 25

aaa ggt cgc aga ggc cag agg ggc aaa aat cgg ggg tgc gtc tta act 435  
 Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr  
 30 35 40

gca ata cac tta aat gtc act gac ttg ggt ttg ggc tac gaa acc aag 483  
 Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys  
 45 50 55 60

gag gaa ctg atc ttt cga tat tgt agc ggt tcc tgt gaa gcg gcc gag 531  
 Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu  
 65 70 75

aca atg tac gac aaa ata cta aaa aat ctg tct cga agt aga agg cta 579  
 Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu  
 80 85 90

aca agt gac aag gta ggc cag gca tgt tgc agg ccg gtc gcc ttc gac 627  
 Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp  
 95 100 105

gac gac ctg tcg ttt tta gac gac agc ctg gtt tac cat atc cta aga 675  
 Asp Asp Leu Ser Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg  
 110 115 120

aag cat tcc gct aaa cgg tgt gga tgt atc tgaccctggc tccagagact 725  
 Lys His Ser Ala Lys Arg Cys Gly Cys Ile  
 125 130

gctgtgtatt gcattcctgc tacactgcga agaaagggac caaggttccc aggaaatatt 785

tgcccagaaa ggaagataag gaccaagaag gcagaggcag aggcggaaga agaagaagaa 845

aagaaggacg aaggcagcca tctgtgggag cctgtagaag gaggcccagc tacag 900

<210> 4

<211> 227

<212> PRT

<213> Rattus rattus

<400> 4

Val Tyr Gly Asp Arg Ile Arg Gly Ala Ala Ala Gly Arg Asp Ser Lys  
 -90 -85 -80

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr  
 -75 -70 -65

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Leu Leu Glu Ala Pro  
 -60 -55 -50

Ala Glu Asp His Ser Leu Gly His Arg Arg Val Pro Phe Ala Leu Thr  
 -45 -40 -35 -30

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val  
 -25 -20 -15

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp  
 -10 -5 -1 1

Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala  
 5 10 15

Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg  
 20 25 30 35

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr  
 40 45 50

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr  
 55 60 65

Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp Lys Ile Leu  
 70 75 80

Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln  
 85 90 95

Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp  
 100 105 110 115

Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys  
 120 125 130

Gly Cys Ile

<210> 5

<211> 562

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (24)..(506)

&lt;223&gt;

&lt;220&gt;

&lt;221&gt; mat\_peptide

&lt;222&gt; (105)..()

&lt;223&gt;

&lt;400&gt; 5

|   |     |
|---|-----|
| attttctctt ttctttttga aca agc aat atg cca gag gat tat cct gat cag | 53  |
| Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln                           |     |
| -25 -20   |     |
| ttc gat gat gtc atg gat ttt att caa gcc acc att aaa aga ctg aaa   | 101 |
| Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys   |     |
| -15 -10 -5  |     |
| agg tca cca gat aaa caa atg gca gtg ctt cct aga aga gag cgg aat   | 149 |
| Arg Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn   |     |
| -1 1 5 10 15  |     |
| cgg cag gct gca gct gcc aac cca gag aat tcc aga gga aaa ggt cgg   | 197 |
| Arg Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg   |     |
| 20 25 30  |     |
| aga ggc cag agg ggc aaa aac cgg ggt tgt gtc tta act gca ata cat   | 245 |
| Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His   |     |
| 35 40 45  |     |
| tta aat gtc act gac ttg ggt ctg ggc tat gaa acc aag gag gaa ctg   | 293 |
| Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu   |     |
| 50 55 60  |     |
| att ttt agg tac tgc agc ggc tct tgc gat gca gct gag aca acg tac   | 341 |
| Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr   |     |
| 65 70 75  |     |
| gac aaa ata ttg aaa aac tta tcc aga aat aga agg ctg gtg act gac   | 389 |
| Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Thr Asp   |     |
| 80 85 90 95   |     |
| aaa gta ggg cag gca tgt tgc aga ccc atc gcc ttt gat gat gac ctg   | 437 |
| Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu   |     |
| 100 105 110   |     |
| tcg ttt tta gat gat aac ctg gtt tac cat att cta aga aag cat tcc   | 485 |
| Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser   |     |
| 115 120 125   |     |

gct aaa agg tgt gga tgt atc tgactccggc tccagagact gctgtgtatt 536  
 Ala Lys Arg Cys Gly Cys Ile  
 130

gcattcctgc tacagtgcaa agaaag 562

<210> 6

<211> 161

<212> PRT

<213> Homo sapiens

<400> 6

Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp  
 -25 -20 -15

Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln  
 -10 -5 -1 1 5

Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Ala  
 10 15 20

Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys  
 25 30 35

Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu  
 40 45 50

Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser  
 55 60 65

Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn  
 70 75 80 85

Leu Ser Arg Asn Arg Arg Leu Val Thr Asp Lys Val Gly Gln Ala Cys  
 90 95 100

Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn  
 105 110 115

Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys  
 120 125 130

Ile

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide probe

<220>

<221> misc\_feature

<222> (3)..(3)

<223> N at position 3 is inosine

<220>

<221> misc\_feature

<222> (15)..(15)

<223> N at position 15 is inosine

<220>

<221> misc\_feature

<222> (18)..(18)

<223> N at position 18 is inosine

<400> 7

ccngayaarc argcngcngc

20

<210> 8

<211> 223

<212> DNA

<213> Homo sapiens

<400> 8

ttctctcccc cacctccgc ctgcccgcgc aggtgccgcc gccggacggg actttaagat 60  
gaagttatgg gatgtcgtgg ctgtctgcct ggtgctgctc cacaccgcgt ccgccttccc 120  
gctgcccgcc ggtaagaggc ctcccagggc gcccgccgaa gaccgctccc tcggccgccc 180



ccgcgcgccc ttgcgctga gcagtgactg taagaaccgt tcc 223

<210> 9

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide linker

<400> 9  
cccgaattcg gg

12

<210> 10

<211> 7

<212> PRT

<213> Rattus rattus

<400> 10

Pro Asp Lys Gln Ala Ala Ala  
1 5

<210> 11

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleic acid sequence from pBluescript SK-76.1 encoding rat GDNF  
N-terminus sequence

<400> 11  
gagaggaacc ggcaagctgc wgmwgywmwgm ccw

33

<210> 12

<211> 11

<212> PRT

<213> Rattus rattus

<400> 12

Glu Arg Asn Arg Gln Ala Ala Ala Ser Pro  
1 5 10

<210> 13

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Oligonucleotide PCR primer DHD-26 to amplify DNA encoding rat GDN  
F polypeptide

<220>

<221> misc\_feature

<222> (9)..(9)

<223> N at position 9 is inosine

<220>

<221> misc\_feature

<222> (12)..(12)

<223> N at position 12 is inosine

<400> 13

arrttyttna rnatytrtc

20

<210> 14

<211> 7

<212> PRT

<213> Rattus rattus

<220>

<221> misc\_feature

<223> Internal rat GDNF peptide

<400> 14

Asp Lys Ile Leu Lys Asn Leu  
1 5

<210> 15

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD1 to amplify rat GDNF probe

<400> 15  
gacgggactc taagatg

17

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer DHD23 to amplify rat GDNF probe

<220>

<221> misc\_feature

<222> (3)..(3)

<223> N at position 3 is inosine

<220>

<221> misc\_feature

<222> (6)..(6)

<223> N at position 3 is inosine

<220>

<221> misc\_feature

<222> (18)..(18)

<223> N at position 3 is inosine

<400> 16

gcngcngcyt gyttrtcngg

20

<210> 17

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer LF2 to amplify rat GDNF probe

<400> 17

cgagacaatg tacgaca

17

<210> 18

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD2 to amplify rat GDNF probe

<400> 18

ctctggagcc aggtca

17

<210> 19

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD1 to amplify rat GDNF probe

<400> 19

cccgaattcg acgggactct aagatg

26

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer LFA to amplify rat GDNF probe

<400> 20

cggtggccag agggagtggc ctcc

24

<210> 21

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD3 to amplify human cDNA

<400> 21

cgcggtacca ataaggagga aaaaaaatgt caccagataa acaaat

46

<210> 22

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer PD4 to amplify human cDNA

<400> 22

cgcggtaccc agtctctgga gccgga

26

<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic adapter fragment for plasmid pCJ1

&lt;400&gt; 23

gatctagaat tgatcatgttt gacagcttat cat

33

&lt;210&gt; 24

&lt;211&gt; 37

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Polylinker sequence for plasmid pCJX1-1 with EcoRI and PSTI overhangs

&lt;400&gt; 24

aattcccggtg taccagatct gagctcacta gtctgca

37

&lt;210&gt; 25

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (32)..(691)

&lt;223&gt;

&lt;220&gt;

&lt;221&gt; mat\_peptide

&lt;222&gt; (290)..()

&lt;223&gt;

&lt;400&gt; 25

ttctctccccc cacctcccgcc ctgcccgccg a ggt gcc gcc gcc gga cgg gac  
Gly Ala Ala Ala Gly Arg Asp  
-85 -80

52

|   |     |
|---|-----|
| ttt aag atg aag tta tgg gat gtc gtg gct gtc tgc ctg gtg ctg ctc | 100 |
| Phe Lys Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu |     |
| -75 -70 -65   |     |
| cac acc gcg tcc gcc ttc ccg ctg ccc gcc ggt aag agg cct ccc gag | 148 |
| His Thr Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu |     |
| -60 -55 -50   |     |
| gcg ccc gcc gaa gac cgc tcc ctc ggc cgc cgc cgc gcg ccc ttc gcg | 196 |
| Ala Pro Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala |     |
| -45 -40 -35   |     |
| ctg agc agt gac tca aat atg cca gag gat tat cct gat cag ttc gat | 244 |
| Leu Ser Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp |     |
| -30 -25 -20   |     |
| gat gtc atg gat ttt att caa gcc acc att aaa aga ctg aaa agg tca | 292 |
| Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser |     |
| -15 -10 -5 -1 1   |     |
| cca gat aaa caa atg gca gtg ctt cct aga aga gag cgg aat cgg cag | 340 |
| Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln |     |
| 5 10 15   |     |
| gct gca gct gcc aac cca gag aat tcc aga gga aaa ggt cgg aga ggc | 388 |
| Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly |     |
| 20 25 30  |     |
| cag agg ggc aaa aac cgg ggt tgt gtc tta act gca ata cat tta aat | 436 |
| Gln Arg Gly Lys Asn Arg Cys Val Leu Thr Ala Ile His Leu Asn     |     |
| 35 40 45  |     |
| gtc act gac ttg ggt ctg ggc tat gaa acc aag gag gaa ctg att ttt | 484 |
| Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe |     |
| 50 55 60 65   |     |
| agg tac tgc agc ggc tct tgc gat gca gct gag aca acg tac gac aaa | 532 |
| Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys |     |
| 70 75 80  |     |
| ata ttg aaa aac tta tcc aga aat aga agg ctg gtg act gac aaa gta | 580 |
| Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Thr Asp Lys Val |     |
| 85 90 95  |     |
| ggg cag gca tgt tgc aga ccc atc gcc ttt gat gat gac ctg tgc ttt | 628 |
| Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe |     |
| 100 105 110   |     |
| tta gat gat aac ctg gtt tac cat att cta aga aag cat tcc gct aaa | 676 |
| Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys |     |
| 115 120 125   |     |
| agg tgt gga tgt atc tgactccggc tccagagact gctgtgtatt gcattcctgc | 731 |
| Arg Cys Gly Cys Ile   |     |
| 130   |     |
| tacagtgcaa agaaag   | 747 |

&lt;210&gt; 26

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Homo.sapiens

&lt;400&gt; 26

Gly Ala Ala Ala Gly Arg Asp Phe Lys Met Lys Leu Trp Asp Val Val  
 -85 -80 -75

Ala Val Cys Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro  
 -70 -65 -60 -55

Ala Gly Lys Arg Pro Pro Glu Ala Pro Ala Glu Asp Arg Ser Leu Gly  
 -50 -45 -40

Arg Arg Arg Ala Pro Phe Ala Leu Ser Ser Asp Ser Asn Met Pro Glu  
 -35 -30 -25

Asp Tyr Pro Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr  
 -20 -15 -10

Ile Lys Arg Leu Lys Arg Ser Pro Asp Lys Gln Met Ala Val Leu Pro  
 -5 -1 1 5 10

Arg Arg Glu Arg Asn Arg Gln Ala Ala Ala Asn Pro Glu Asn Ser  
 15 20 25

Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val  
 30 35 40

Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu  
 45 50 55

Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala  
 60 65 70

Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg  
 75 80 85 90

Arg Leu Val Thr Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Ile Ala  
 95 100 105

Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr His Ile  
 110 115 120

Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile  
 125 130



&lt;210&gt; 27

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Rattus rattus

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;223&gt; Rat pre-pro GDNF

&lt;400&gt; 27

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr  
1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Leu Leu Glu Ala Pro  
20 25 30

Ala Glu Asp His Ser Leu Gly His Arg Arg Val Pro Phe Ala Leu Thr  
35 40 45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val  
50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp  
65 70 75 80

Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala  
85 90 95

Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg  
100 105 110

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr  
115 120 125

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr  
130 135 140

Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp Lys Ile Leu  
145 150 155 160

Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln  
165 170 175

Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp  
 180 185 190

Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys  
 195 200 205

Gly Cys Ile  
 210

<210> 28

<211> 211

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<223> Human pre-pro GDNF

<400> 28

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr  
 1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro  
 20 25 30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser  
 35 40 45

Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val  
 50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp  
 65 70 75 80

Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala  
 85 90 95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg  
 100 105 110

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr  
 115 120 125

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr  
 130 135 140

Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu  
 145 150 155 160

Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Thr Asp Lys Val Gly Gln  
 165 170 175

Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp  
 180 185 190

Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys  
 195 200 205

Gly Cys Ile  
 210

<210> 29

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Human pre-pro GDNF N-terminal fragment

<400> 29

Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr  
 1 5 10 15

Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro  
 20 25 30

Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser  
 35 40 45

Ser Asp  
 50